

FIGURE 1

GGACTAATCTGTGGGAGCAGTTTATTCCAGTATCACCCAGGGTGCAGCCACACCAGGACTGT
GTTGAAGGGTGTTTTTTTCTTTAAATGTAATACCTCCTCATTTTCTTCTTACACAGTG
TCTGAGAACATTTACATTTAGATAAGTAGTACATGGTGGGATAACCTTCTACTTTTAGGAGGA
CTACTCTCTTCTGACAGTCTCTAGACTGGTCTTCTACACTAAGACACC**ATGA**AGGAGTATGTG
CTCTATTATTCTGGCTTTGTGCTCTGCCAAACCCCTTCTTTAGCCCTTCACACATCGCACT
GAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATGATG
ATGATGATGATGAGGACAACCTCTCTTTTCCAAACAGAGAGCCAAAGAGCCATTTTTCCTCA
TTTGATCTGTTTTCCAATGTGTCCATTTGGATGTCAGTGTCTATTCCAGAGTTGTACATTTGCTC
AGATTTAGGTTTGACCTCAGTCCCAACCAACATTTCCATTTGATACTCGAATGCTTGATCTTC
AAAACAATAAAATTAAGGAAATCAAAGAAAATGATTTTAAAGGACTCACTTCACTTTATGGT
CTGATCCTGAACAACAACAAGCTAACGAAGATTCAACCCAAAGCCCTTCTAACCACAAAGAA
GTTGCGAAGGCTGTATCTGTCCACAATCAACTAAGTGAATACCACCTTAATCTTCCCAAAT
CATTAGCAGAAGCTCAGAATTCATGAAAATAAAGTTAAGAAAATACAAAAGGACACATTTCAA
GGAAATGAATGCTTTACACGTTTTGGAAATGAGTGCAAAACCTCTTGATAATAATGGGATAGA
GCCAGGGGCATTTGAAGGGGTGACGGTGTTCATATCAGAATTCGAGAAGCAAAACCTGACCT
CAGTTCTTAAAGGCTTACCACCAACTTTATTGGAGCTTCACTTAGATTATAATAAAATTTCA
ACAGTGGAACCTTGAGGATTTTAAACGATACAAAGAAGCTACAAAGGCTGGGCCTAGGAAACAA
CAAAATCACAGATATCGAAAATGGGAGTCTTGCTAACATACCAGTGTGAGAGAAAATACATT
TGGA AAAACAATAACTAAAAAAAATCCCTTCAGGATTAACAGAGTTGAATAGCTCCAGATA
ATCTTCCTTCATTCTAATTCAATTGCAAGAGTGGGAGTAAATGACTTCTGTCCAACAGTGCC
AAAGATGAAGAAATCTTTATACAGTGCAATAAGTTTATTCAAACAACCCGGTGAATACTGGG
AAATGCAACCTGCAACATTTCTGTTGTGTTTTGAGCAGAATGAGTGTTCAGCTTGGGAACCTT
GGAATG**TA**ATAATTAGTAATTGGTAATGTCCATTTAATAATAAGATTCAAAAATCCCTACATT
TGGAATACTTTGAACCTATTATAATATGGTAGTATTATATATACAAGCAAATATCTATTCTCA
AGTGGTAAGTCCACTGACTTATTTTATGACAAGAAATTTCAACGGAATTTTGCCAAACTATT
GATACATAAGGGGTTTGAGAGAAACAAGCATCTATTGCAGTTTCTTTTTCGCTACAAATGAT
CTTACATAAATCTCATGCTTGACCATTCCTTTCTTCATAACAAAAAGTAAGATATTCGGTA
TTTAAACACTTTTGTTATCAAGACATTTTAAAAAGAAGCTGTACTGTAAATGGAATGCTTGACT
TAGCAAAATTTGTTCTTTCTTCAATTGCTGTGTAGAAAAACAGAATTAACAAAGACAGTAATGT
GAAGAGTGCATTACACTATTCTTATTCTTTAGTAACTTGGGTAGTACTGTAAATATTTTAAAT
CATCTTAAAGTATGATTTGTATATAATCTTATTGAAATTACCTATCATGCTCTTAGAGCCCGT
CTTTATGTTTAAAACTAATTTCTTAAAAATAAGCCCTTCAGTAAATGTTTCATTACCAACTTGA
TAAATGCTACTATAAGAGCTGGTTTGGGGCTATAGCATATGCTTTTTTTTTTTTAAATATT
ACCTGATTTAAAAATCTCTGTAAAAACGTGTAGTGTTCATAAAATCTGTAACCTCGCATTTT
AATGATCCGCTATTATAAGCTTTTAAATAGCATGAAAATTTGTAGGCTATATAACATTGCCAC
TTCACCTCTAAAGGAATATTTTGGAGATATCCCTTTGGAAGACCTTGCTTGGAAAGAGCTGGA
CACTAACAAATCTACACCAAAATTTGCTCTTCAAATACGTATGGACTGGATAACTCTGAGAAA
CACATCTAGTATAACTGAATTAAGCAGAGCATCAAAATAAACAGACAGAAACCGAAAGCTCTTA
TATAAATGCTCAGAGTTCTTTATGTATTCTTATGGCATTCACATATGTAATAATCAGAAA
ACAGGGAAATTTTCATTAAAAATATTGGTTTGAAAT

FIGURE 2

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34392

<subunit 1 of 1, 379 aa, 1 stop

<MW: 43302, pI: 7.30, NX(S/T): 1

MKEYVLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDEDNSLFPTREPR
SHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGL
TSLYGLILNNNKLTKIHPKAFLT¹TKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKI²Q
KDTFKGMNALHVLEMSANPLDNNGIEPGA³FE⁴GVTVFHIRIAEAKLTSVPKGLPPTLLELHLD
YNKISTVELED⁵FKRYKELQRLGLGNNKITDIENGLANIPRVREIHLENNKLKKIPSGLP⁶EL
KYLQII⁷IFLHSNSIARVGVND⁸FCPTVPKMKSLYSAISLFNNPVKYWEMQ⁹PATFRCVLSRMSV
QLGNFGM

Signal sequence.

amino acids 1-15

N-glycosylation site.

amino acids 281-285

N-myristoylation sites.

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

Leucine zipper pattern.

amino acids 154-176

FIGURE 3

CGGACGCGTGGGCGGACGCGTGGGCCGCGSGCACCGCCCCCGGCCCGGCCCTCCGGCTCCGCACTCGCGCCTCC
 CTCCTCCGGCCGCGTCCGCGGCCCTCTCTCCCTCCTCCAGCTGTCCGGTTCGGGTATGCGGAGCGCTCC
 GGCCCCCGCGGCCCGCTGCTGCTCTCGGGCTGCTGCTGCTCGGCTCCCGCGCGGCCCGCGCGGCCCGCCAGA
 GCCCCCGCTGCTGCCATCCGTCTTCTGAGAAGGAGCCGCTGCCCGTTCGGGGAGCGGCAAGCTGCACCTTCGGCGG
 GAAGGTCTATGCTTGGACGAGACGTGGCACCCGGACCTAGGGCAGCCATTTCGGGGTGATGCGCTGCGTGTGTG
 CGCCTCGGAGGCGCCTCAGTGGGGTGC CGCTACAGGGGCCCTGGCAGGGTCACTGCAAGAACTCAAAACCGAGA
 GTGCGCAACCCCGGCTGTGGGCGAGCCGCGCAGCTGCGGGACACTGCTGCGCAGACCTGCCCCAGAGCGCGAG
 CAGTTTCGGAGCGGACGCGAGCGGCCCTGTCTTCGAGTATCCGCGGGACCCGGAGCATCGAGCTTTATAGGACCG
 CGGGAGACGAGCGCTGAGGAGCGGGCCCGTGGTGACCGGCACACGGACTCTGGCGCTGACAGAGGCGGAG
 GTCGCAAGCGGTGGCACGAGCCCGAGTCTCGCTGCTGCGCTCTAGCCTCCGCTTCTCTATCTCTACAGGCGGCT
 GGACGCCCTACCCAGGATCCGCTTCTCAGACTCCAATGGCAGTGTCTGTGTTGAGCACCTGCAAGCCCCACCCA
 AGATGGCTGGTCTGTGGGGTGTGGCGGGCAGTGCCCTCGGTTGTCTCTGCGGCTCCTTAGGGCAGAAGACTGCA
 GTGGCACTTGTGACACTCACTACCTTTCAGGGGAGGCTGTGGGGCTCTCATCCGCGACCGGGCCCTGGCTGC
 AGAGACCTTTCAGTGCCATCTGACTCTAGAAGGCCCCCAAGCGGCGTACAGGGGATACACCTTGCTCACTCT
 CAGTGACACAGAGGACTCCTTGCAATTTTTTGTCTGCTCTTCGAGGGCTGCTGGAACCCAGGAGTGGGGGACTAAC
 CCAGGTTCCCTTAGGCTTCAGATTCTACACAGGGGCGAGCTACTGCGAGAACTTCAGGCCAATGTCTCAGCCCA
 GGAAACAGGCTTTTGTGAGGTGTCTGCCCACTGACAGTCCAGGAGATGGAGTGGTGTCTGGGGGAGCTGCA
 GATGCGCCTGGAGTGGGACAGGCGCAGGGCTGCGCATCAGTGACACATCTGCGCGCAGGAGAGCTGCGACGT
 CTGCGAAAGTGTCTTTGTGGGGCTGATGCCCTGATCCCACTCAGAGGGGTGCTGCGGCTCAGGCCAGCTCAGC
 GCTGTAGGAAATGGCTCCCTGATCTATCAGGTGCAAGTGTAGGGACAAGCAGTGAAGTGGTGGCCATGACACT
 GGAGACCAAGCCTCAGCGGAGGGATCAGCGCACTGTCTGTGCCACATGGCTGAGCTCCAGCCAGGAGGACACAC
 GGCGTGGGTATCTGCCCTGGGCTGGGTGCCCGAGGGGCTCATATGCTGTGAGAAATGAGCTCTTCTGAAAGCT
 GGGCACCAAGGACTTCCAGACGGAGAGCTTCGGGGGCGAGTGGCTGCCCTGCCCTACTGTGGGCATAGCGCCCG
 CCATGACACGCTGCCCTGCCCGCTTAGCAGGAGCCCTGGTGTACCCCTGTGAAGAGCAAGCAGCAGGAGGACGC
 CTGGGTTTCTTGGATACCCACTGTCACTGCACTATGAAGTGTCTGTGGCTGGGCTGGTGGCTCAGAGCAAGG
 CACTGTCACTGCCCACTCTTGGGGCTCCTGGAACGCCAGGGCTCGGGGCTGTGTAAGGATTTCTATGGCTC
 AGAGGCCCAAGGCTGTGGTGAAGGACCTGGAGCCGGAAGTGTGCGGCACCTGGCAAAAGGATGGCTCCCTGAT
 GATCACCAAGGGTAGCCCCAGAGGGGAGCTCCGAGGGCAGGTGCACATAGCCAACCAATGTGAGGTTGGCGG
 ACTGCGCTGGAGGCGGCGGGGCGAGGGGGTGGCGGCTGGGGGCTCCGGATACAGCCTCTGCTGCGCGGCC
 TGTGTGCTGTGCTCTCCGCGCCTAGCGCCCGGCAAACTGGTGTCTTGGGCGGCCCGAGACCCCAACACATG
 CTCTCTTGGAGGGGCGAGCGCGCCCCACGGGGCTGCTGGGCGGCCAACTACGACCCGCTCTGCTCACTCTGCAC
 CTGCGAGAGACAAAGGTGATCTGTGACCCGGTGGTGTGCCACCGCCAGCTGTGCCACACCCGGTGCAGGCTCC
 CGACCAGTGTGCTCTGTTTGGCTGAGAAACAAGATGTGAGAGCTTGCAGGGCTGCCAAGGAGCGGGGACCC
 AGGAGAGGGCTGCTATTTTGTATGGTACCGGAGCTGGCGGGCAGCGGCTACGCGGTGGCACCCCGTTGTGGCCCC
 CTTTGGCTTAATTAAGTGTGCTGTGCACTTGAAGGGGGGCACTGGAGAGGTGCACTGTGAGAAGGTGCACTGT
 TCCCGGCTGGCTGTGCCCCAGCCTGTGCGTGTCAACCCCAAGCTGTGCAAGAGGGTGTCAAGTGGGGTGGG
 GGCCACACCCAGCTGGGGAGCCCATGCGAGGCTGATGGGCCCGGGGCTGGCGTTTGTGTGGGAGTGGTCCC
 AGAGAGTCAGAGCTGGACACCCCTCAGTGCCCCCTTTTGGAGAGATGAGCTGTATCACTGTCAGATGTGGGGGAG
 GGTGCTCACTGTGAGCGGGATGACTGTTCACTGCCACTGTCTGTGGCTCGGGGAAGGAGATCGATGCTGTTCT
 CGCTGCAAGGCCACCGGCGGGCCCCAGAGACCAGAACTGATCTCAGAGCTGGAGAAAGAGCGGAAGGCTCTTA
 GGGAGCAGCCAGAGGGCCAACTGACCAAGAGGATGGGGGCTGAGCTGGGAGAGGGGTGGCATCGAGGACCTCTT
 GCATTCTCTGTGGGAAGCCAGTGCTTTGTCTCTGTCTGCTCTACTCCCAACCCCACTCACTCTGGGAA
 CCACAGCTCCAGAGGGGAGAGCGAGCTGGGCGACAGCGAGTCAAGGTCACAGCTCTGCGCTGCCACCC
 TCGGCTCTGTCTGGAAGCCCCACCCCTTTCTCTGTACATAATGTCAGTGGCTTGTGGGATTTTAAATTTA
 TCTTCACTAGCACCAAGGGCCCCGACACTCACTCCTGCTGCCCTGAGCTGAGCAGAGTCATTATTGGAGAG
 TTTTGTATTTATTAACAATTTCTTTTCAGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

bioRxiv preprint doi: <https://doi.org/10.1101/111111>; this version posted November 1, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

FIGURE 4

><subunit 1 of 1, 954 aa, 1 stop

><MW: 101960, pI: 8.21, NX(S/T): 5

MPSPAPPAPALLLLGLLLGSRPARGAGPEPPVLPPIRSEKEPLPVRGAAGCTFGGKVYALDE
TWHFDLQPPFGVMRCVLCACEAPQWGRRTRGPRVSCNKKPECPTPACGQPRQLPGHCCQT
CPQERSSSERQPSGLSFEYPRDPEHRSYSDRGEPGAEEERAGDGHDTDFVALLTGPRSQAVAR
ARVSLLRSSLRFSISYRRDRPRTIRFSDSNGSVLFEHPAAPTQDGLVCGVWRVAPRLSLRL
LRAEQLHVALVTLTHPSGEVWGPIRHRALAAETFSAILTLEGPPQGGVGGITLLTSDTED
SLHFLLLFRGLLEPRSGGLTQVPLRLQILHQQLLRELQANVSAQEPGFAEVLPNLTVQEMD
WLVLGELQMALEWAGRPGRLRISGHIAARKSCDVLQSVLCGADALIPVQTGAAGSASLTLLGN
GSLIYQVQVVGTSSEVVAMTLETKEPQRDQRTVLCMHAGLQPGGHTAVGICPGLGARGAHL
LQNELFLNVGTDKFPDGLRGHVAALPYCGHSARHDTLPVPLAGALVLPVKSAAGHAWLS
LDTHCHLHYEVLLAGLGGSEQGTVTAHLGPPGTPGPRLLKGFYGSEAQGVKDLPEPELLR
HLAKGMASLMITTKGSPRGELRGQVHIANQCEVGGRLLEAAGAEVVRALGAPDTASAAPPVV
PGLPALAPAKPGGPRPRDPNTCFEFGQQRPHGARWAPNYDPLCSLCTCQRRTVICDPVVC
PPSCPHPVQAPDQCCPVCEKQDVRLDPLGPRSRDPGEGCYFDGDRSWRAAGTRWHPVVPF
GLIKCAVCTCKGGTGEVHCQKQCPRLACAQPVVNPTDCKQCPVGSAGHPQLGDPMQADG
PRGCRFAGQWFFPESQSWHPSVPPFGEMSCITCRGAGVPHCERDDCSLPLSCGSGKESRCCS
RCTAHRPPPETRTDPELEKEAEGS

Signal sequence.

amino acids 1-23

N-glycosylation sites.

amino acids 217-221, 351-355, 365-369, 434-438

Tyrosine kinase phosphorylation sites.

amino acids 145-153, 778-786

N-myristoylation sites.

amino acids 20-26, 47-53, 50-56, 69-75, 73-79, 232-238, 236-242,
390-396, 422-428, 473-479, 477-483, 483-489, 489-495, 573-579,
576-582, 580-586, 635-641, 670-676, 773-779, 807-813, 871-877,
905-911

Amidation site.

amino acids 87-91

Cell attachment sequence.

amino acids 165-168

Leucine zipper pattern.

amino acids 315-337

FIGURE 5

GGCGGAGCAGCCCTAGCGCCACCGTCGCTCTCGCAGCTCTCGTCGCCACTGCCACCGCGCGCGCTCACTGCG
TCTTGGCTCGGGCTCCGCGGCCCTCCGCGCGGCCA**ATGC**AGCCCCGCGCGCAGGCGCCCGGTGCGCAGCTGC
TGCCCGCGCTGGCCCTGCTGCTGCTGCTGCTCGGAGCGGGGCCCCGAGGCGAGCTCCCTGGCCAAACCGGTGCGCG
CGCGCGCCTTGTCTGCGGCCGCGCGCTGCGCGCGCAGCCCTGCCGGAATGGGGGTGTGTGCACCTTGCAGCCCTG
AGCGCGACCCGAGCACC CGGCCCGCGCGCGAGCTGGCTACAGCTGCACCTGCCCGCGCGGATCTTCGCGCG
CCAACCTGCCAGCTTGTTCAGATTCCTTGTGCCAGCAACCTTGTACCATGGCAACTGCAGCAGCAGCAGCAGCA
GCAGCAGCAGTACCTTACCTTGCATTTCGAATGAAGGCTATGAAGTCCCAACTGTGAACAGGCACCTTCCAGTGC
TCCACAGCCATGGCTGGACGAATCCATGGCACC CGGACAGCTTCAGCCCTGTTCTGTCTACTCAGGAGCTTGACA
AAATCTGCCTGCCTCTCAGGCAACGGTGACACTGCCTACCTGGCAGCCGAAAAAGGCGCAAAAGTTGTAGAAA
TGAAATGGGATCAAGTGGAGTGATCCAGATATTGCTGTGGGAATGCCAGTTCTTAACAGCTCTCGGGGTGGCC
GCCTGGTATCCTTTGAAGTGCCACGAAACCTCAGTCAAGATTTCGGAAGATGCCACTGCCTCACTGATTTTTC
TCTGGAAGGTCACGGCCACAGGATTCACACAGTGCTCCCTCATAGATGGACGAAGTGTGACCCCGCTTCAGGCTT
CAGGGGGAGCTGGTCCCTCCTGGAGGAGATGCTCGCTTGGGGAATTAATCACTTTATTGGTTTTGTGAATGATTTCTG
TGACTAAGTCTATTGTGGCTTTGCGCTTAACCTTGGTGGTGAAGGTGACAGCTGTGTGCGCGGGGAGAGTGCAG
CAAATGACTTGGAGTGTTTCAGGAAAAGGAAATGCACACGAAAGCCGTGAGGAGCACTTTTCTCTGTACCTGTG
AGGAGCAGTACGTGGGTACTTCTTGTGAAGAATACGATGCTTGGCAGAGAACTTGCACAAAACACACGCGAGCT
GTATTGATGCAAAATGAAGAGCAAGATGGGAGCAATTTACCTGTGTTTGCTTCTCGTTATACTGGAGAGCTTT
GCCAGTCCAAGATTGATTACTGCATCTAGACCCATGCAGAAATGGAGCAACATGCATTTCCAGTCTCAGTGGAT
TCACCTGCGAGTGTCCAGAGGATACTTCCGATCTGCTTGTGAAGAAAAGGTGGACCCCTGCGCTCTCGTCTCCGT
CGCAGAACACCGGCACCTGCTATGTGGACGGGTGACACTTTACCTGCAACTGCAGCCCGGGCTTCACAGGGCCGA
CCTGTGCCAGCTTTATTGACTTCTGTGGCTTCAGCCCTGTGCTCATGGCAGCTGCCGACGCTGGGCAACAGCT
ACAAATGCCTCTGTGATCCAGGTTACCATGGCTCTACTGTGAGGAGGAATATAATGAGTGCCTCTCCGCTCCAT
GCCTGAATGCAGCCACCTGCAGGGACCTCGTTAATGGCTATGAGTGTGTGCTTGGCAGGAATACAAAGGAACAC
ACTGTGAATTGTACAAAGATCCCTGCGCTAACGTCAGCTGTCTGAACGGAGCCACCTGTGACAGCGACGCGCTGA
ATGGCAGTGCACTGTGTCACCCGGGTTTACAGGTGAAGAGTGGCACTTGACATAAATGAATGTGACAGTAACC
CCTGCCACCATGGTGGGAGCTGCCTGGACAGCCCAATGGTTATAACTGCGCCAGCTGGCTTGGTGGGAG
CAAACTGTGAGATCCACCTCCAATGGAAGTCCGGGCACATGGCGGAGAGCCTCACCAACTGCCACGGCACCTCCC
TCTACATCATCATTTGGAGCCCTCTGCGTGGCTTCATCCTTATGCTGATCATCTGCATGTGGGATTTTGGCGCA
TCAGCCCGATTGAATACCGAGGTTTTCAGGCGAGCCTATGAGGAGTTCTACAACCTGCCGAGCATCGACAGCG
AGTTTCAGCAATGCCATTGCATCCATCCGGCATGCCAGGTTTGGAAAGAAATCCCGGCTCGCAATGTATGATGTGA
GCCCATCGCTATGAAGATTACAGTCTGATGACAAACCTTGGTCACTAGTAAAACTAAAGATTGT**TAAT**
CTTTTTTGGATTATTTTCAAAAAGATGAGATACTACACTCATTTAAATATTTTTAAGAAAAATAAAAGCTTAA
GAAATTTAAATAGCTAGCTGCTCAAGAGTTTTTCACTAGAATATTTAAGAACTAAATTTCTGCAGCTTTTAGTTTG
GAAAAATATTTTAAAAACAAATTTTGTGAACCTATAGACGATGTTTAAATGTACCTTCAGCTCTCTAAACTGT
GTGCTTCTACTAGTGTGTGCTCTTTTCACTGTAGACACTATCACGAGACCCAGATTAAATTTCTGTGGTTGTACA
GAATAAGTCAATCAAGGAGAGTTTCTGTTTGACGTTTGAGTGCCGCTTCTGAGTAGAGTTAGGAAACCAAC
GTAAAGTATGATATGATGATAATAGAGTATACCGTTACTTAAAAAGAAAGTCTGAATGTTCTGTTTGTGGAAA
AGAAACTAGTTAAATTTACTATTCTTAACCGAATGAATTAGCCTTTGCCCTTATCTGTGTCATGGGTAAAGTAAC
TTATTTCTGCAGCTGTTTGTGTAACCTTGTGGAACATTCTTCGAGTTTGTTTTGTCAATTTCTGAACAGTGC
TCGAAC TAGGCCCTAAAAACATACGTAACGAAAAGGCCCTAGCGAGGCAAAATCTGATTGATTGAACTATATTT
TCTTTAAAAAGTACAGGTTCTATATTTGTGAGTAAATAAATTTCAATTTAGTGTGTTTGTGGTGTGAAGAGTAG
TAAATGTAAAGAGTACTGGTTCCTTCAGTAGTGAGTATTTCTCATAGTCAGCTTTATTTATCTCCAGGATGTT
TTTGTGGCTGTATTTGATTGATATGTGCTTCTTGATCTTGCTAATTTTCAACCATATTGAATAAATGTGATC
AGTCA

FIGURE 6

><subunit 1 of 1, 737 aa, 1 stop

><MW: 78475, pI: 5.09, NX(S/T): 11

MQPRRAQAPGAQLLPALALLLLLLLGGAGPRGSSSLANPVPAAPLSAPGPCAAQPCRNGGVCTSR
PEPDPQHPAPAGEPGYSTCTPAGISGANCLVADPCASNPCHHGNCSSSSSSSDGYLCICN
EGYEGNPCEQALPSLPATGWTESMAPRQLQVPVATQEPDKILPRSQATVTLPTWQPKTGQKV
VEMKWDQVEVIPDIACGNASSNSSAGGRLVSFEVPQNTSVKIRQDATASLILLWKVTATGFQ
QCSLIDGRSVTPLQASGGVLLEEMALGNNHFIGFVNDSVTKSIVALRLTLVVKVSTCVPG
ESHANDLECSGKGKCTTKPSEATFSCTCEEQYVGTFCEEYDACQRKPCQNNASCIDANEKQD
GSNFTCVCLPGYTGELCQSKIDYCIIDPCRNATCISLSGFTQCCEPGYFGSACEKEVDPC
ASSPCQNNGTCTYVDGVHFTCNCSPGFTGPTCAQLIDFCALSPCAHGTCRSVGTSTYKCLCDPG
YHGLYCEEEYNECLSAFCILNAATCRDLVNGYECVCLAELYKTHCELYKDPANVSCLNGATC
DSDGLNGTICAPGFTGEEDIDINECDSPCHHGSCLDQPNNGYNCHCPHGWWGANCEIHL
QWKS GHMAESLTNMPRHSYIIIGALCVAFILMLIILIVGICRISRIEYQGSRRPAYEEFYN
CRSIDSEFSNAIASIRHARFGKSRPAMYDVSPAIYEDYSPDDKPLVTLIKTKDL

Signal sequence.

amino acids 1-28

Transmembrane domain.

amino acids 641-660

N-glycosylation sites.

amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,
375-379, 442-446, 549-553, 564-568

Glycosaminoglycan attachment site.

amino acids 320-324

Tyrosine kinase phosphorylation sites.

amino acids 490-498, 674-682

N-myristoylation sites.

amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,
373-379, 449-455, 480-486, 562-568, 565-571

Amidation site.

amino acids 702-706

Aspartic acid and asparagine hydroxylation site.

amino acids 520-532, 596-608

EGF-like domain cysteine pattern signatures.

amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,
491-503, 529-541, 567-579, 605-617

FIGURE 7

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCCTTTCAGGCCTTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATA
ATCACTTTATTGGTTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTAAC
CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAATGACTTGGAGTGTTT
AGGAAAAGGAAAATGCACCACGAAGCCGTCAGAGGCAACTTTTTCTGTACCTGTGAGGAGC
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAC
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTGTTGCCTTCC
TGTTTATACTGGAGAGCTTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT
GAGATAGGGGAG

1000
900
800
700
600
500
400
300
200
100
0

FIGURE 8

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCCTTTCAGGCCTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATA
ATCACTTTATTGGTTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTAACT
CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAATGACTTGGAGTGTTT
AGGAAAAGGAAAATGCACCACGAAGCCGTCAGAGGCAACTTTTTCCTGTACCTGTGAGGAGC
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAC
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCTTCC
TGGTTATACTGGAGAGCTTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT
GAGATAGGGGAG

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100

FIGURE 5

GCTGAGTCTGCTGCTCCTGCTGCTGCTGCTCCAGCCTGTAACCTGTGCCTACACCACGCCAG
GCCCCCCAGAGCCCTCACCACGCTGGGCGCCCCAGAGCCACACCATGCCGGGACCTAC
GCTCCCTCGACCACACTCAGTAGTCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGGCCCT
GATGCGGGACTTCCCGCTCGTGGACGGCCACAACGACCTGCCCTTGGTCCTAAGGCAGGTTT
ACCAGAAAGGGCTACAGGATGTTAACCTGCGCAATTTCAGCTACGGCCAGACCAGCCTGGAC
AGGCTTAGAGATGGCCTCGTGGGCGCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCA
GGACCGGGATGCCCTGCGCCTCACCTGGAGCAGATTGACCTCATACGCCGATGTGTGCCT
CCTATTCTGAGCTGGAGCTTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCC
TGCTCATCGGTGTAGAGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTT
CTACATGCTGGGAGTGCCTACCTGACGCTCACCCACACCTGCAACACACCTGGGCAGAGA
GCTCCGCTAAGGGCTCCACTCCTTCTACAACAACATCAGCGGGCTGACTGACTTTGGTGAG
AAGGTGGTGGCAGAAATGAACCGCCTGGGCATGATGGTAGACTTATCCCATGTCTCAGATGC
TGTGGCACGGCGGGCCCTGGAAGTGTACAGGCACCTGTGATCTTCTCCACTCGGTGCCCC
GGGTGTGTGCAACAGTCTCGGAATGTTCTGATGACATCCTGCAGCTTCTGAAGAAGAAC
GGTGGCGTGTGATGGTGTCTTTGTCCATGGGAGTAATACAGTGCAACCCATCAGCCAATGT
GTCCACTGTGGCAGATCACTTCGACCACATCAAGGCTGTCAATTGGATCCAAGTTCATCGGGA
TTGGTGGAGATTATGATGGGGCCGGCAAATCCCTCAGGGGCTGGAAGACGTGTCCACATAC
CCGGTCTGATAGAGAGTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCTT
TCGTGGAAAACCTGCTGCGGGTCTTCAGACAAGTGGAAAAGGTACAGGAAGAAACAAATGGC
AAAGCCCCCTTGAGGACAAGTTCCTCGGATGAGCAGCTGAGCAGTTCTGCCACTCCGACCTC
TCACGTCTGCGTCAGAGACAGAGTCTGACTTCAGGCCAGGAACCTCACTGAGATTCCCATACA
CTGGACAGCCAAGTTACAGCCAAGTGGTCAGTCTCAGAGTCTCCCCCACATGGCCCCAG
TCCTTGCACTGTGGCCACCTTCCAGTCCTTATTCTGTGGCTCTGATGACCCAGTTAGTCC
TGCCAGATGTCACTGTAGCAAGCCACAGACACCCCAAAAGTCCCCCTGTTGTGCAGGCACA
AATATTTCTGAAATAAATGTTTGGACATAG

FIGURE 10

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35595

<subunit 1 of 1, 433 aa, 1 stop

<MW: 47787, pI: 6.11, NX(S/T): 5

MPGTYAPSTTLSSPSTQGLQEQRALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIRMCASYSELELVTSAKALND
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNNGGVVMVSLSMGVIQCNPSPANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE
DVSTYFVLIEELLSRGWSEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS
CHSDLSRLRQRQSLTSGQELTEPIHWTAKLPKWSVSESSPHMAPVLAVVATFPVLILWL

N-glycosylation sites.

amino acids 58-62, 123-127, 182-186, 273-277

N-myristoylation sites.

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

Renal dipeptidase active site.

amino acids 134-157

FIGURE 11

AAAACTATAAATATTCCGATTATTATACACGTCCACCATCGGGCGCGGATCCGCGGCCG
CGAATTCTAAACCAACATGCCGGGCACCTACGCTCCCTCGACCACACTCAGTAGTCCCAGCA
CCCAGGGCCTGCAAGAGCAGGCACGGGCCCTGATCGGGGACTTCCCCTCGTGGACGGCCAC
AACGACCTGCCCCCTGGTCTTAAGGCAGGTTTACCAGAAAGGGCTACAGGATGTTAACCTGCG
CAATTTCAGCTACGGCCAGACCAGCCTGGACAGGCTTAGAGATGGCCTCGTGGGCGCCCAGT
TCTGGTCAGCCTATGTGCCATGCCAGACCAGGACCGGGATGCCCTGCGCCTCACCTGGAG
CAGATTGACCTCATACGCCGCATGTGTGCCTCCTATTCTGAGCTGGAGCTTGTGACCTCGGC
TAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCTCATCGGTGTAGAGGGTGGCCACTCGC
TGGACAATAGCCTCTCCATCTTACGTACCTTCTACATGCTGGGAGTGCCTACCTGACGCTC
ACCCACACCTGCAACACACCCCTGGGCAGAGAGCTCCGCTAAGGGCGTCCACTCCTTCTACAA
CAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGTGGCAGAAATGAACCGCCTGGGCA
TGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGCGGGGCCCTGGAAGTGTACAG
GCACCTGTGATCTTCTCCCACTCGGCTGCCCCGGGTGTGTGCAACAGTGCTCGGAATGTTCC
TGATGACATCCTGCAGCTTCTGAAGAAGAACGGTGGCGTCGTGATGGTGTCTTTGTCCATGG
GAGTAATACAGTGCAACCCATCAGCCAAATGTGTCCACTGTGGCAGATCACTTCGACCACATC
AAGGCTGTCAATGGATCCAAGTTCATCGGGATTGGTGGAGATTATGATGGGGCCGGCAAATT
CCCTCAGGGGCTGGAAGACGTGTCCACATACCCGGTCTGATAGAGGAGTTGCTGAGTCTGTG
GCTGGAGTGAGGAAGAGCTTCAGGGTGTCTTCGTGAAACCTGCTGCGGGTCTTCAGACAA
GTGGAAGAGGTACAGGAAGAAAAAATAATGGCAAAGCCCCCTTGGAGGACAAGTTCCCGGATGA
GCAGCTGAGCAGTTCTGCCACTCCGACCTCTCAGTCTGCGTCAGAGACAGAGTCTGACTT
CAGGCCAGGAACCTACTGAGATTCCCATACACTGGACAGCCAAGTTACCAGCCAAGTGGTCA
GTCTCAGAGTCTCCCCCACCCTGACAAAACCTCACACATGCCACCGTGCCCGACACCTGA
ACTCTGGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCAAGGACACC

FIGURE 12

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA35872
><subunit 1 of 1, 446 aa, 0 stop
><NX(S/T): 5
MPGTYPSTTSSPSTQGLQEQRALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIRMCASYSELELVTSAKALND
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNNGVVMVSLSMGVIQCNPNSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE
DVSTYFVLIEELLSRGWSEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS
CHSDLSRLRQRQSLTSGQELTEIP IHWTAKLPAKWSVSESSPHDPKTHTCP PCAPELLGGP
SVFLFPPKPKDT
```

FIGURE 13

CGCCAGCGACGTGCGGGCGGCCTGGCCCGCGCCCTCCCGCGCCCGGCTGCGTCCCGCGCC
CTGCGCCACCGCCGCGGAGCCGAGCCCGCGCGCCCGCGGAGCGCCGCGCCCGCCATGCCCC
GCCGGCCGCGCGGGGCCCCCGCCGCCAATCCGCGCGGCGGCGCGCGGTGTGTCGCCCTGCT
GCTGTGCTCTGCGTCTCTCGGGCGCGCGAGCCGGATCAGGAGCCACACAGCTGTGATCA
GTCCCCAGGATCCCACGCTTCTCATCGGCTCCTCCCTGTGCGCCACCTGCTCAGTGACGGGA
GACCCACCAGGAGCCACCGCGGAGGGCCTCTACTGGACCTCAACGGGCGCGCGCTGCCCCCC
TGAGCTCTCCCGTGTACTCAACGCTCCACCTTGGCTCTGGCCCTGGCCAACTCAATGGGT
CCAGGCAGCGGTGCGGGGACAACCTCGTGTGCCACGCCGTGACGGCAGCATCCTGGCTGGC
TCTGCTCTATGTTGGCTGCCCGCAGAGAAACCGTCAACATCAGTGCTGGTCCAAGAA
CATGAAGGACTTGACCTGCCGTGGACGCCAGGGGCCCCAGGGGAGACCTTCTCCACACCA
ACTACTCCCTCAAGTACAAGCTTAGGTGGTATGGCCAGGACAACACATGTGAGGAGTACCAC
ACAGTGGGGCCCCACTCTGCCACATCCCCAAGGACCTGGCTCTCTTTACGCCCTATGAGAT
CTGGGTGGAGGCCACCAACCGCTGGGCTCTGCCGCTCCGATGTACTCACGCTGGATATCC
TGGATGTGGTGACCACGACCCCCCGCGACGTGCACGTGAGCCGCGTGGGGGCTGGAG
GACCAGCTGAGCGTGGCTGGGTGTGCCACCCGCCCTCAAGGATTTCTCTTTCAAGCCAA
ATACCAGATCCGCTACCGAGTGGAGGACAGTGTGGACTGGAAGTGGTGGACGATGTGAGCA
ACCAGACCTCCTGCCGCTGGCCGGCCTGAAACCCGGCACCGTGTACTTCGTGCAAGTGC
TGCAACCCCTTTGGCATCTATGGCTCCAAGAAAGCGGGATCTGGAGTGAGTGGAGCCACCC
CACAGCCGCTCCACTCCCCGAGTGAGCGCCCGGGCCCGGGCGCGGGGCGTGCGAACCGC
GGGGCGGAGAGCCGAGCTCGGGGCGGTGCGGCGCGAGCTCAAGCAGTTCTGGGCTGGCTC
AAGAAGCACGCGTACTGCTCCAACCTCAGCTTCGCGCTCTACGACCAGTGGCGAGCCTGGAT
GCAGAAGTCGCACAAGACCCGCAACCAGGACGAGGGGATCTGCCCTCGGGCAGACGGGGCA
CGCGAGAGGTCTGTCAGATTAAGCTGTAGGGGCTCAGGCCACCTCCTGCCACGTGGAGA
CGCAGAGGCCGAACCCAACTGGGGCCACCTCTGTACCTCACTTCAGGGCACCTGAGCCAC
CCTCAGCAGGAGCTGGGGTGGCCCTGAGCTCCAACGCCATAACAGCTCTGACTCCACGT
GAGGCCACCTTTGGGTGCACCCAGTGGGTGTGTGTGTGTGTGAGGGTTGGTTGAGTTGC
CTAGAACCCCTGCCAGGGCTGGGGGTGAGAAGGGGAGTCATTACTCCCCATTACCTAGGGCC
CCTCCAAAAGAGTCTTTTAAATAAATGAGCTATTTAGGTGCTGTGATTGTGAAAAA
AAA

FIGURE 14

><ss.DNA38113
><subunit 1 of 1, 422 aa, 1 stop
><MW: 46302, pI: 9.42, NX(S/T): 6
MPAGRRGPAAQSARRPPLPLPLLLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATCSV
HGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSIL
AGSCLYVGLPPEKPVNISCSKNMKDLTCRWTPGAHGETFLHTNYSLKYLKRWYQDNTCEE
YHTVGPCHSHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDVHVS RVGG
LEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDKVVDVSNQTSCLAGLKP GTVYFVQ
VRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSGPPVRRELKQFLG
WLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGPAR

Signal sequence.

amino acids 1-30

Transmembrane domain.

amino acids 44-61

N-glycosylation sites.

amino acids 92-96, 104-108, 140-144, 168-172, 292-296, 382-386

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 413-417

N-myristoylation sites.

amino acids 30-36, 37-43, 73-79, 121-127, 179-185, 218-224,
300-306, 317-323, 320-326, 347-353, 355-361, 407-413

Amidation site.

amino acids 3-7, 79-83, 411-415

Growth factor and cytokines receptors family signature 2.

amino acids 325-331

FIGURE 15

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCCTCTAAAGCAGTTTAGAGTGGTAAAAAA
AAAAAAAAACACACCAACGCTCGCAGCCACAAAGGGATGAAATTTCTTCTGGACATCCTC
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTTCGTGAAGCTTTTTATTCTCTAA
GAGGAGAAAATCAGTCACCGCGGAAATCGTGTGATTACAGGAGCTGGGCATGGAATTGGGA
GACTGACTGCCTATGAATTTGCTAAACTTAAAGCAAGCTGGTTCCTCTGGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTCATACCTTTGT
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGACATTTCTGGACTACAAA
GGCATTTCCTTCTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG
CTGGACATGTCTCGTCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGTCTGTGTTGGA
TTTCATAAAACTTTGACAGATGAACTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATG
TCTGTGTCTTAATTCGTAAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCA
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG
ATTTTATTCCATCTTCTATAGCTTTTTTAACAACATTGGAAAGGATCCTTCCTGAGCGTTT
CCTGGCAGTTTTAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATTGGATATAAAATGA
AAGCGCAATAAGCACCTAGTTTTCTGAAAACGATTACCAGGTTTAGGTTGATGTCATCTA
ATAGTGCCAGAATTTAATGTTTGAACCTTCTGTTTTTCTAATTATCCCCATTTCTTCAATA
TCATTTTGGAGGCTTTGGCAGTCTTCATTTTACTACCACTTGTTCTTTAGCCAAAAGCTGATT
ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAGAA
CCAAAATGACTTTATTAAATAATTTCCAAGATTATTGTGGGCTCACCTGAAGGCTTTGCAA
AATTTGTACCATAACCGTTTATTAAACATATATTTTATTTTGTATTGCACTTAAATTTGT
ATAATTTGTGTTTCTTTTCTGTTCTACATAAAATCAGAAACTTCAAGCTCTCTAAATAAAA
TGAAGGACTATATCTAGTGGTATTTCAATGAATATCATGAACCTCTCAATGGGTAGGTTTC
ATCTACCCATTGCCACTCTGTTTCTGAGAGATACCTCACATTCCAATGCCAAACATTTCT
GCACAGGGAAGCTAGAGGTGGATACACGTGTGCAAGTATAAAAGCATCACTGGGATTAAAG
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA
AA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 16

</usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA34436

<subunit 1 of 1, 300 aa, 1 stop

<MW: 32964, pI: 9.52, NX(S/T): 1

MKFLLDILLLLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKKVKAIEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTASAAGHVSVPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDDAIGYKMKQAQ

Signal sequence.

amino acids 1-19

Transmembrane domain.

amino acids 170-187

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 30-34, 283-287

N-myristoylation sites.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 17

GA CTAGT TCTCTTGGAGTCTGGGAGGAGGAAAGCGGAGCCGGCAGGGAGCGAACCAGGACTG
GGGTGACGGCAGGGCAGGGGGCGCCTGGCCGGGGAGAAGCGCGGGGGCTGGAGCACCACCAA
CTGGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGGGGGACT
GCGAGAGGACCCCGCGTCCGGGCTCCCGGTGCGAGCGCTATGAGGCCACTCCTCGTCTCTGC
TGCTCTTGGGCTTGGCGCGCGGCTCGCCCCACTGGACGACAACAAGATCCCCAGCCTCTGC
CCGGGGCACCCCGGCTTCCAGGCACGCGGGCCACCATGGCAGCCAGGGCTTGCCGGGGCCG
CGATGGCCCGACGGCCGCGACGGCGCGCCCGGGGCTCCGGGAGAGAAAGGCGAGGGCGGGA
GGCCGGGACTGCCGGGACCTCGAGGGGACCCCGGGCCGCGAGGAGAGGCGGGACCCGCGGGG
CCCAACGGGCTGCCGGGGAGTGCTCGGTGCCTCCGCGATCCGCCTTCAGCGCCAAGCGCTC
CGAGAGCCGGGTGCCTCCGCGCTTGACGCACCCTTGCCCTTCGACCGCGTGCTGGTGAACG
AGCAGGGACATTACGACGCCGTACCGGCAAGTTCACCTGCCAGGTGCCTGGGGTCTACTAC
TTCGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGAATGGCGA
ATCCATTGCCTCTTTCTTCCAGTTTTTTCGGGGGTGGCCCAAGCAGCCTCGCTCTCGGGGG
GGGCCATGGTGAGGCTGGAGCCTGAGGACCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTAC
ATTGGCATCTATGCCAGCATCAAGACAGACAGCACCTTCTCCGATTCTGGTGTA CTCCGA
CTGGCACAGCTCCCCAGTCTTTGCTTAGTGCCCCACTGCAAAGTGAGCTCATGCTCTCACTCC
TAGAAGGAGGGTGTGAGGCTGACAACCAGGTCATCCAGGAGGGCTGGCCCCCTGGAATATT
GTGAATGACTAGGGAGGTGGGGTAGAGCACTCTCCGTCCTGTGCTGGCAAGGAATGGGAAC
AGTGGCTGTCTGCGATCAGGTCTGGCAGCATGGGGCAGTGGCTGGATTCTGCCCAAGACCA
GAGGAGTGTGCTGTGCTGGCAAGTGAAGTCCCCCAGTTGCTCTGTGTCAGGAGCCCAAGGT
GGGTGCTCTCTTCTGCTCTCTGCTTCTCTGGATCCTCCCCACCCCTCTGCTCCTGGG
GCCGGCCCTTTTCTCAGAGATCACTCAATAAACCTAAGAACCTCATAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

FIGURE 18

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40592

><subunit 1 of 1, 243 aa, 1 stop

><MW: 25298, pI: 6.44, NX(S/T): 0

MRPLLVLALLGLAAGSPPLDDNKIPSLCPGHPGLPGTTPGHHSQGLPGRDGRDGRDGAPGAP
GEKGEGRPGPLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLP
FDRVLVNEQGHYDAVTGKFTCQVPGVYFVAVHATVYRASLQFDLVKNGESIASFFQFFGGWP
KPASLSGGAMVRLEPEDQVWVQVGVDYIGIYASIKTDSTFSGFLVYSDWHSSPVFA

Signal sequence.

amino acids 1-15

N-myristoylation sites.

amino acids 11-17, 68-74, 216-222

Cell attachment sequence.

amino acids 77-80

FIGURE 19

CTCTTTTGTCCACCAGCCAGCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTGAG
AAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCAACAGACCCAT
GCTGCATCCAGAGACCTCCCCTGGCCGGGGGCATCTCCTGGCTGTGCTCCTGGCCCTCCTTG
GCACCACCTGGGCAGAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCC
CTGAACAGGAAGGAGAGTTTCTTGCTCCTCTCCCTGCACAACCGCCTGCGCAGCTGGGTCCA
GCCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCAACTGGCTCAAG
CCAGGGCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCCCTG
CAAGTGGGCTGGAACATGCAGCTGTGCCCCGCGGCTTGGCGTCCTTTGTTGAAGTGGTCAG
CCTATGGTTTGCAGAGGGGCAGCGGTACAGCCACGCGGCAGGAGAGTGTGCTCGCAACGCCA
CCTGCACCCACTACACGCAGCTCGTGTGGGCCACCTCAAGCCAGCTGGGCTGTGGCGGCAC
CTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCTGTGCCTACTCCCCGGAGGCAA
CTGGGAGGTCAACGGGAAGACAATCATCCCCTATAAGAAGGGTGCCCTGGTGTTGCTCTGCA
CAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCATGCAGGGGGGCTCTGTGAGGTCCCC
AGGAATCCTTGTGCGATGAGCTGCCAGAACCATGGACGTCTCAACATCAGCACCTGCCACTG
CCACTGTCCCCCTGGCTACACGGGCAGATACTGCCAAGTGAGGTGCAGCCTGCAGTGTGTGC
ACGGCCGGTTCCGGGAGGAGGAGTGTCTGTCGCTCTGTGACATCGGCTACGGGGGAGCCAG
TGTGCCACCAAGGTGCATTTTCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTT
CATGGTGTCTTCAAGGCAGACACCTATTACAGAGCCAGGATGAAATGTCAGAGGAAAGGCG
GGGTGCTGGCCCCAGATCAAGAGCCAGAAAGTGCAGGACATCCTCGCCTTCTATCTGGGCCGC
CTGGAGACCACCAACGAGGTGACTGACAGTGACTTCGAGACCAGGAACCTTCTGGATCGGGCT
CACCTACAAGACCGCCAAGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTACCA
GTTTTGCCTTTTGGGCAGCCTGACAACACGGGCTGGTGTGGCTGAGTGCTGCCATGGGGTTT
GGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCTTCAACTGGAACGACCAGCGCTGCAAAAC
CCGAAACCGTTACATCTGCCAGTTTGCCAGGAGCACATCTCCCGTGGGGCCAGGGCTCCT
GAGGCCTGACCACATGGCTCCCTCGCCTGCCCTGGGAGCACCGGCTCTGCTTACCTGTCTGC
CCACCTGTCTGGAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCCAAGAGGTCTCAGA
CCTTGCACAATGCCAGAAGTTGGGCAGAGAGAGGACGGGAGGCCAGTGAGGGCCAGGGAGTG
AGTGTTAGAAGAAGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGA
TGCGCAAGGAGAGGACACCGCCAGTGGTCCAAAAAGGCTGCTCTCTTCCACCTGGCCAGAC
CCTGTGGGGCAGCGAGCTTCCCTGTGGCATGAACCCACGGGGTATTAAATTATGAATCAG
CTGAAAAAAAAAAAA

FIGURE 20

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44176

<subunit 1 of 1, 455 aa, 1 stop

<MW: 50478, pI: 8.44, NX(S/T): 2

MLHPETSPGRGHLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRSWV
QPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVV
SLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCASAGQTAIEAFVCAYSPGG
NWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSQCNHGRLNISTCH
CHCPPGYTGRYCQVRCSLQCVHGRFREBECSVCVDIGYGGAQCATKVHFPFHTCDLRIDGDC
FMVSSEADTYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLTNEVTDSDFETRNFwig
LTYKTAKDSFRWATGEHQAFTSFAGQPDNHGLVWLSAAMGFGNCVELQASAAFNWNDQRCK
TRNRYICQFAQEHISRWGPgs

Signal sequence.

amino acids 1-26

Transmembrane domain.

amino acids 110-124

N-glycosylation sites.

amino acids 144-148, 243-247

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 45-49

N-myristoylation sites.

amino acids 22-28, 99-105, 131-137, 201-207, 213-219, 287-293,
288-294, 331-337, 398-404

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 204-215

EGF-like domain cysteine pattern signature.

amino acids 249-261, 280-292

C-type lectin domain signature.

amino acids 417-442

FIGURE 21

CGGACGCGTGGGCTGGGCGCTGCAAAGCGTGTCCCGCCGGTCCCCGAGCGTCCCGCGCCCT
CGCCCCGCGC**ATG**CTCCTGCTGTGGGGCTGTGCCCTGGGGCTGTCCCTGTGTGTGGGGTGCA
GGAAGAGGCGCAGAGCTGGGGCCACTCTTCGGAGCAGGATGGACTCAGGGTCCCGAGGCAAG
TCAGACTGTTGCAGAGGCTGAAAACCAAACCTTTGATGACAGAATTCTCAGTGAAGTCTACC
ATCATTTCGGTTATGCCCTTCACTACGGTTTCCTGCAGAAATGCTGAACAGAGCTTCTGAAGA
CCAGGACATTGAGTTCAGATGCAGATTCAGCTGCAGCTTTTCATCACCAACTTCACTATGC
TTATTGGAGACAAGTGTATCAGGGCGAAATTACAGAGAGAGAAAAGAAGAGTGGTGATAGG
GTAAAAGAGAAAAAGGAATAAAACCAAGAAGAAAATGGAGAGAAGGGGACTGAAATATTTCAG
AGCTTCTGCAGTGATTCACAGCAAGGACAAAGCCGCCTTTTTCCTGAGTTATGAGGAGCTTC
TGCAGAGGCGCTGGGCAAGTACGAGCACAGCATCAGCGTGCAGGCCCGCCAGCAGCTGTCCGGG
AGGCTGAGCGTGGACGTGAATATCCTGGAGAGCGCGGGCATCGCATCCCTGGAGGTGCTGCC
GCTTCACAACAGCAGGCAGAGGGGCGAGTGGGCGCGGGGAAGATGATTCTGGGCCCTCCCCCAT
CTACTGTCATTAAACCAAAATGAAACATTTGCCAACATAATTTTTAAACCTACTGTAGTACAA
CAAGCCAGGATTGCCCAAGATGGAATTTTGGGAGACTTTATCATTAGATATGACGTCAATAG
AGAACAGAGCATTGGGGACATCCAGGTTCTAAATGGCTATTTTGTGCACTACTTTGCTCCTA
AAGACCTTCTCCTTTACCAAGAATGTGGTATTCTGTGCTTGACAGCAGTGCTTCTATGGTG
GGAACCAAACTCCGCGACAGCAAGGATGCCCTCTTCACAATCTCCATGACCTCCGACCCCA
GGACCGTTTCAGTATCATTGGATTTTCCAACCGGATCAAAGTATGGAAGGACCACCTTGATAT
CAGTCACTCCAGACAGCATCAGGGATGGGAAAGTGACATTACCATATGTCAACCACCTGGA
GGCACAGACATCAACGGGGCCCTGCAGAGGGCCATCAGGCTCCTCAACAAGTACGTGGCCCA
CAGTGGCATTGGAGACCGGAGCGTGTCCCTCATCGTCTTCTGACGGGATGGGAAGCCCAAGG
TCGGGGAGACGCACACCCTCAAGATCCTCAACAACACCCGAGAGGCCGCCGAGGCCAAGTC
TGCACTTACCATTGGCATCGGCAACGACGTGGACTTCAGGCTGCTGGAGAAACTGTCGCT
GGAGAACTGTGGCCTCACACGGCGCGTGCACGAGGAGGAGGACGAGGCTCGCAGCTCATCG
GGTTCTACGATGAAATCAGGACCCCGCTCCTCTCTGACATCCGATCGATTATCCCCCAGC
TCAGTGTGCGAGGCCACCAAGACCTGTTCCCCAACTACTTCAACGGCTCGGAGATCATCAT
TGCGGGGAAGCTGGTGGACAGGAAGCTGGATCACCTGCACGTGGAGGTACCGCCAGCAACA
GTAAGAAATTCATCATCCTGAAGACAGATGTGCCTGTGCGGCCCTCAGAAGGCAGGGAAAGAT
GTCACAGGAAGCCCCAGGCCTGGAGGCGATGGAGAGGGGGACCAACCCATCGAGCGTCT
CTGGAGCTACCTCACCACAAGGAGCTGCTGAGCTCCTGGCTGCAAAGTGACGATGAACCGG
AGAAGGAGCGGCTGCGGCAGCGGGCCAGGCCCTGGCTGTGACCTACCGCTTCTCACTCCC
TTCACTCTCATGAAGCTGAGGGGGCCGGTCCCACGCATGGATGGCCTGGAGGAGGCCACGG
CATGTGCGCTGCCATGGGACCCGAACCGGTGGTGCAGAGCGTGCAGGAGCTGGCACGCAGC
CAGGACCTTTGCTCAAGAAAGCCAAACTCCGTCAAAAAAAGCAAAAAAAGAAAGAA
CATGGGAGAGATGTTGTTTTTCTCTCCACCACCTGGGGATACGAT**TGA**GAGATGGCCACCT
CCAAGCCAGGAAGACGGCCCTCACCAGACCATGTCTGCTGGCACCTTGATCTTGGACCTC
CGAGCTTCAGAACTGTGAGAAATAAATGTGTTTTGTTTAAGCTAAAAAAGAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 22

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44192

<subunit 1 of 1, 694 aa, 1 stop

<MW: 77400, pI: 9.54, NX(S/T): 6

MLLLLGLCLGLSLCVGSQEEAQSWGHSSEQDGLRVPRQVRLLQRLKTKPLMTEFSVKSTIIIS
RYAFTTVSCRMNLNRASEDQDIEFQMQUIPAAAFITNFTMLIGDKVYQGEITEREKKSGDRVKE
KRNKTTEENGEKGTEIFRASAVIPSKDKAAFFLSYEELLQRRLGKYEHSISVRPQQLSGRLS
VDVNILESAGIASLEVLPLHNSRQRGSGRGEDDSGPPSTVINQNETFANIIFKPTVVQQAR
IAQNGILGDFIIRYDVNREQSIGDIQVLNGYFVHYFAPKDLPLPKNVVFLDSSASMGVTK
LRQTKDALFTILHDLRPQDRFSIIGFSNRIKVWKDHLISVTPDSIRDGKVYIHHMSPTGGTD
INGALQRAIRLLNKYVAHSGIGDRSVSLIVFLTDGKPTVGETHTLKI LNNTREAAARGQVCIF
TIGIGNDVDFRLLLEKLSLENCGLTRRVHEEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVV
QATKTLFPNYFNGSEII IAGKLVDKLDHLHVEVTASNSKKFII LKTDVPVRPQKAGKDV TG
SPRPGGDGEGDTNHIERLWSYLTTKELLSSWLQSDDEPEKERLRQRAQALAVSYRFLTPPTS
MKLRGPVPRMDGLEEAHGMSAAMGPEPVVQSVRGAGTQPGPLLKKPNSVKKKQNKTKKRHGR
DGVFPLHHLGIR

Signal sequence.

amino acids 1-14

N-glycosylation sites.

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

Glycosaminoglycan attachment sites.

amino acids 213-217, 391-395

N-myristoylation sites.

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

FIGURE 23

CGGACGCGTGGGGTGCCCGACATGGCGAGTGTAGTGCTGCCGAGCGGATCCCAGTGTGCGGC
GGCAGCGGCGGCGGCGGCGCTCCCGGGCTCCGGCTTCTGCTGTTGCTCTTCTCCGCGCGG
CACTGATCCCCACAGGTGATGGGCAGAAATCTGTTTACGAAAGACGTGACAGTGATCGAGGGA
GAGGTTGCGACCATCAGTTGCCAAGTCAATAAGAGTGACGACTCTGTGATTAGCTACTGAA
TCCCAACAGGCAGACCATTTATTTTCAGGGACTTCAGGCCTTTGAAGGACAGCAGGTTTCAGT
TGCTGAATTTTTCTAGCAGTGAACCTCAAAGTATCATTGACAAACGCTCTCAATTTCTGATGAA
GGAAGATACTTTTGCCAGCTCTATACCGATCCCCACAGGAAAGTTACACCACCATCACAGT
CCTGGTCCCACCACGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGG
AGATTGAAGTCAACTGCATGCTATGGCCAGCAAGCCAGCCACGACTATCAGGTGGTTCAAA
GGGAACACAGAGCTAAAAGGCAAATCGGAGGTGGAAGAGTGGTCAGACATGTACACTGTGAC
CAGTCAGCTGATGCTGAAGGTGCACAAGGAGGACGATGGGGTCCCAGTGATCTGCCAGGTGG
AGCACCTGCGGTCACTGGAAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCT
CAAGTGCACATTGAGATGACTTATCCTCTACAAGGCTTAACCCGGGAAGGGGACGCGCTTGA
GTTAACATGTGAAGCCATCGGGAAGCCCCAGCCTGTGATGGTAACTTGGGTGAGAGTCGATG
ATGAAATGCCTCAACACGCGTACTGTCTGGGCCAACCTGTTTCATCAATAACCTAAACAAA
ACAGATAATGGTACATACCGCTGTGAAGCTTCAAACATAGTGGGGAAAGCTCACTCGGATTA
TATGCTGTATGTATACGATCCCCCACAACATATCCCTCCTCCCACAACAACCACCACCACCA
CCACCACCACCACCACCACCATCCTTACCATCATCAGATTCCCGAGCAGGTGAAGAAGGC
TCGATCAGGGCAGTGGATCATGCCGTGATCGGTGGCGTCTGTGGCGTGGTGGTGTTCGCCAT
GCTGTGCTTGCTCATCATTTCTGGGGCGCTATTTTGCCAGACATAAAGGTACATACTTCACTC
ATGAAGCCAAAGGAGCCGATGACGCAGCAGACGCAGACACAGCTATAATCAATGCAGAAGGA
GGACAGAACAACCTCCGAAGAAAAGAAAGAGTACTTCATCTAGATCAGCCTTTTGTGTTCAAT
GAGGTGTCCAACCTGGCCCTATTTAGATGATAAAGAGACAGTGATATTGG

FIGURE 24

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518
<subunit 1 of 1, 440 aa, 1 stop
<MW: 48240, pI: 4.93, NX(S/T): 7
MASVVLPSGSQCAAAAAAAAAAPPGLRLLLLLFSAAALIPTGDGQNLF TKDVTVIEGEVATISC
QVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSELKVSLTNVSI SDEGRYFCQL
YTDPPQESYTTITVLVPPRNL MIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKG
KSEVEEWSDMYTVTSQMLMLKVHKEDDGVFVICQVEHPAVTGNLQTQRYLEVQYKPVH IQMT
YPLQGLTREGDALELTCEAIGKPQPMVTWVRVDDEMPQHAVLSGPNLFINN LNKTDNGTYR
CEASNIVGKAHSDYMLYVYDPPTTIPPTTTTTTTTTTTTTTTILTIITDSRAGEEGSIRA VDH
AVIGGVAVVVFAMLCLLIILGRYFARHKGTFTHEAKGADDAADADTAIINAEGGQNNSEE
KKEYFI

Signal sequence.

amino acids 1-36

Transmembrane domain.

amino acids 372-393

N-glycosylation sites.

amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310,
430-434

Tyrosine kinase phosphorylation sites.

amino acids 233-240, 319-328

N-myristoylation sites.

amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,
411-417, 427-433, 428-432

FIGURE 25

GGGGCGGGTGGACGCGGACTCGAAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGA
 CCGCGCAGGAAGAGCTGAGGCCGCGGCTTGCCTCGCCGCGCTCCCTGGCGCGCGCGCGCTC
 CCGGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCTCTGCTACTGGCCCT
 GGGGCCCTGGGGTGCAGGGCTGCCCATCCGGTGCAGTGCAGCCAGCCACAGACAGTCTTCT
 GCACTGCCCCGCCAGGGGACCAGGTGCCCGAGACGTGCCACCCGACACGGTGGGGCTGTAC
 GTCTTTGAGAACCGCATCACATGCTCGACGCAAGCAGCTTTGCCGGCTGCCGGCCCTGCA
 GCTCCTGGACCTGTCAAGAACCAGATCGCCAGCCTGCGCTGCCCGCCTGCTGCTGCTGG
 ACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGACACTGCCAACGTGGAG
 GCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGGGCTCTTCAGCCCGCTTGG
 CAACCTCCACGACCTGGATGTGTCCGACAACCAGCTGGAGCGAGTGCCACCTGTGATCCGAG
 GCCTCCGGGGCTGCAGCGCCTGCGGCTGGCCGGCAACACCCGATTGCCAGCTGCGGGCC
 GAGGACCTGGCCGGCTGGCTGCCCTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGC
 CCTGCCCTGGCGACCTCTCGGGCCTCTTCCCCCGCTGCGGCTGCTGGCAGCTGCCCGCAACC
 CCTTCAACTGCGTGTGCCCCCTGAGCTGGTTTGGCCCTGGGTGCGCGAGAGCCACGTCA
 CTGGCCAGCCCTGAGGAGACGCGCTGCCACTTCCCGCCCAAGAACGCTGGCCGGCTGCTCCT
 GGAGCTTGACTGACGCCACTTTGGCTGCCCGCAGCCACCCACCAAGCCACAGTGCACCA
 CGAGGCCCGTGGTGCAGGAGCCACAGCCTTGTCTTCTAGCTTGGCTCCTACCTGGCTTAGC
 CCGACAGCGCGGCCACTGAGGCCCGCAGCCCGCTCCTGCTGCCACCGACTGTAGGGCC
 TGTCCCCAGCCCGAGGCTGCCACCGTCCACTGCCTCAATGGGGGCACATGCCACCTGG
 GGACACGGCACCACTGGCGTGTCTGTGCCCGAAGGCTTACGCGGCTGTACTGTGAGAGC
 CAGATGGGGCAGGGGACAGGCCAGCCCTACACCAAGTCAAGCCGAGGCCACACGCTCCCT
 GACCCTGGGCATCGAGCCGCTGAGCCCACTCCCTGCGGCTGGGGCTGCAGCGCTACCTCC
 AGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT
 AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACAGGTCAACCAGCTGCG
 GCCAACGCCACTTACTCCGTCTGTGTCATGCCCTTTGGGGCCCGGGCGGGTGCAGGAGGCG
 AGGAGGCTGCGGGGAGGCCCATACACCCCGCCGCTCCACTCCAACACGCCCCAGTCAAC
 CAGGCCCGCGAGGGCAACTGCGCGCTCCTCATTGCGCCCGCCCTGGCGCGGCTGCTCTGGC
 CGCGCTGGCTGCGGTGGGGGCGAGCCTACTGTGTGCGGCGGGGGCGGGCCATGGCAGCAGCGG
 CTCAGGACAAGGGCAGGTGGGGCCAGGGGCTGGGACCTGAGGGAGTGAAGGTC
 CCCTTGGAGCCAGGCCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGTCTGA
 GTGTGAGGTGCCACTCATGGGCTTCCAGGGGCTGGCCTCAGTCAACCTCCACGCAAGC
 CCTACATTAAGCCAGAGAGACAGAGGCGAGTGGGGCGGGCTCTCAGCAGTGAGATGGC
 CAGCCCCCTCTGCTGCCACACCGTAAGTTCTCAGTCCCAACCTCGGGGATGTGTGCAGA
 CAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGACCTCGGTCTCTCATCTGTGAG
 ATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAACCAGTGCTATGAGGACAGTGT
 CCGCCCTGCCCTCCGCAACGTGAGTCCCTGGGCAAGGCGGGCTGCCATGTGTGGTAAC
 GCATGCTGGGGCCTGCTGGGCTCTCCCACTCCAGGCGGACCTTGGGGGCCAGTGAAGGAAG
 CTCGCCGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTGTGACTCTAGTCTTGGCCCCAGG
 AAGGAAGGAACAAAAGAAACTGAAAGGAAGATGCTTTAGGAACATGTTTTGCTTTTTTAA
 AATATATATATATTTATAAGAGATCCTTTCCCATTTATTCTGGGAAGATGTTTTTCAAACCTC
 AGAGACAAGGACTTTGGTTTTTGTAAAGACAAACGATGATATGAAGGCCTTTTGTAAAGAAAA
 ATAAAAAAAAA

FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44804

<subunit 1 of 1, 598 aa, 1 stop

<MW: 63030, pI: 7.24, NX(S/T): 3

MCSRVPLLLLLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGGTTVPRDVPDPTVGLYVFEN
GITMLDASSFAGLPGLQLLDLSQNIASLRRLPRLLLDLSHNSLLALEPGILDATANVEALRL
AGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRLRLAGNTRIAQLRPEDLA
GLAALQELDVSNLSLQALPGDLSGLFPRLRLLLAAARNPFNCVCPLSWFGPWVRESHVTLASP
EETRCHFPFKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTAP
ATEAPSPSTAPPTVGVPVQPQDCPPSTCLNGGTCHLGRHHLACLCEGFTGLYCESQMGQ
GTRPSPTVTPRPPRSLTGIEPVSPSTSLRVGLQRYLQGS SVQLRSLRLTYRNLSGPDKRLV
TLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQARE
GNLPLLIAPALAAVLLAALAAVGAAYCVRGRAMAAAAQDKQGVGPGAGPLELEGVKVPLEP
GPKATEGGGEALPSGSECEVPLMGFPGLQSPLHAKPYI

Signal sequence.

amino acids 1-23

Transmembrane domain.

amino acids 501-522

N-glycosylation sites.

amino acids 198-202, 425-429, 453-457

Tyrosine kinase phosphorylation site.

amino acids 262-270

N-myristoylation sites.

amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

EGF-like domain cysteine pattern signature.

amino acids 355-367

Leucine zipper pattern.

amino acids 122-144, 194-216

FIGURE 27

GGCACTAGGACAACCTTCTTCCCTTCTGCACCACTGCCCGTACCCTTACCCGCCCCGCCACC
TCCTTGCTACCCCACTCTTGAAACCACAGCTGTTGGCAGGGTCCCCAGCTCATGCCAGCCTC
ATCTCCTTTCTTGCTAGCCCCCAAAGGGCCTCCAGGCAACATGGGGGGCCAGTCAGAGAGC
CGGCACTCTCAGTTGCCCTCTGGTTGAGTTGGGGGGCAGCTCTGGGGGCCGTGGCTTGTGCC
ATGGCTCTGCTGACCCAA CAAA CAGAGCTGCAGAGCCTCAGGAGAGAGGTGAGCCGGCTGCA
GGGGACAGGAGGCCCCCTCCAGAATGGGGAAGGGTATCCCTGGCAGAGTCTCCCGAGCAGA
GTTCCGATGCCCTGGAAGCCTGGGAGAATGGGGAGAGATCCCGGAAAAGGAGAGCAGTGCTC
ACCCAAAAACAGAAGAAGCAGCACTCTGTCTCGCACCTGGTTCCCATTAACGCCACCTCCAA
GGATGACTCCGATGTGACAGAGGTGATGTGGCAACCAGCTCTTAGGCGTGGGAGAGGCCTAC
AGGCCCAAGGATATGGTGTCCGAATCCAGGATGCTGGAGTTTATCTGCTGTATAGCCAGGTC
CTGTTTCAAGACGTGACTTTACCATGGGTCAGGTGGTGTCTCGAGAAGGCCAAGGAAGGCA
GGAGACTCTATTCCGATGTATAAGAAGTATGCCCTCCCACCCGACCGGGCTACAAAGCT
GCTATAGCGCAGGTGTCTTCCATTTACACCAAGGGGATATTCTGAGTGTATAATTTCCCGG
GCAAGGGCGAACTTAACCTCTCTCCACATGGAACCTTCTGGGGTTTGTGAACTGTGATT
GTGTTATAAAAAGTGGCTCCAGCTTGGAAGACCAGGGTGGGTACATACTGGAGACAGCCAA
GAGCTGAGTATATAAAGGAGAGGGAATGTGCAGGAACAGAGGCATCTTCTGGGTTTGGCTC
CCCGTTCTCACTTTTCCCTTTTCAATCCACCCCCCTAGACTTTGATTTTACGGATATCTTG
CTTCTGTTCCCCATGGAGCTCCG

FIGURE 28

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52722

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27433, pI: 9.85, NX(S/T): 2

MPASSPFL LAPKGP PGNMG GPVREPALSVALWLSWGAALGAVACAMALLTQQTELQSLRREV
SRLQGTGGPSQNGEGYPWQSLPEQSSDALEAWENGERSRKRRRAVL TQKQKKQHSVLHLVPIN
ATSKDDSDVTEVMWQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTF TMGQVVSREG
QGRQETLFR CIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVII PRARAKLNLSPHGTFLGFVKL

Signal sequence.

amino acids 1-40

N-glycosylation site.

amino acids 124-128

Tyrosine kinase phosphorylation site.

amino acids 156-164

N-myristoylation site.

amino acids 36-42, 40-46, 179-185, 242-248

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 34-45

FIGURE 29

CACTTTCTCCTCTCTTCTTACTTTTCGAGAAACCGCGCTTCCGCTTCTGGTCGCAGAGAC
CTCGGAGACCGCGCCGGGAGACGGAGGTGCTGTGGGTGGGGGGACCTGTGGCTGCTCGTA
CCGCCCCCACCCTCTCTTCTGCACTGCCGTCTTCGGGAAGACCTTTCCCTCTGCTCTGTT
TCCTTACCAGAGTCTGTGCATCGCCCCGGACCTGGCCGGGAGGAGGCTTGGCCGGCGGGAGA
TGCTCTAGGGGGCGCGCGGGAGGAGCGGCCGGCGGGACGGAGGGCCCGGCAGGAAGATGGGC
TCCGTGTGACAGGAGCTTGTGTGGGTACTGCTGCTCTTGGCTTGGCTCTGCTCTGGCTGGT
CCTGAGTCTGTGTCCCCATGTCCAGGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGC
CGTCGCCTCCGGACCATGCGCAGAGGGCTGAAGAAACAATGAAAAATACAGGCCCACTGAG
GACCAGGGGCTCCCTGCTTCCGGTGTCTGCGCTGCTGTGACCCCGGTACCTCCATGTACCC
GGCAGCCGCGGTGCCCCAGATCAACATCACTATCTTGAAGGGGAGAGGGGTGACCGCGGAG
ATCGAGGCCTCAAGGGAAATATGGCAAAACAGGCTCAGCAGGGGCCAGGGGCCACACTGGA
CCCAAAGGGCAGAAGGGCTCCATGGGGGCCCTGGGGAGCGGTGCAAGAGCCACTACGCCGC
CTTTTCGGTGGGCCGGAAGAAGCCCATGCAAGCAACCACTACTACCAGACGGTGATCTTCG
ACACGGAGTTCGTGAACCTCTACGACCACTTCAACATGTTACCCGGCAAGTCTACTGCTAC
GTGCCCGGCTCTACTTCTTTCAGCCTCAACGTGCACACCTGGAAACAGGAAGGAGACCTACT
GCACATCATGAAGAACAGGAGGAGGTGGTGATCTTGTTCGCGCAGGTGGGCGCCAGCA
TCATGCAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACCAGGTGTGGGTACGCCCTC
TACAAGGGCGAACGTGAGAACGCCATCTTCAGCGAGGAGCTGGACACCTACATCACTTTCAG
TGGCTACCTGGTCAAGCACGCCACCGAGCCCTAGCTGGCCGGCCACCTCTTCTCTCTGCC
ACCTTCCACCCTGTGCTGTGTGCTGACCCCAACCGCTCTTCCCGATCTTCCGACTCCGACTC
CCTGGCTTTGGCATTCACTGAGACGCCCTGCACACAGAAAGCCAAAGCATCGGTGCTCC
CAGATCCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACAGGGCGGGGACCCCGC
GAGAACCCTCTGGGACCTTCCGCGGCCCTCTGCAACATCTCAAGTGACCCCGCAGCGC
GAGACGGGGTGGCGGCAGGGCGTCCAGGGTGCGGCACCGCGGCTCCAGTCTTGGAAATA
ATTAGGCAAAATTCTAAAGGTCTCAAAGGAGCAAAGTAAACCGTGGAGGACAAAGAAAAGGG
TTGTTATTTTTTCTTCCAGCAGCCTGCTGGCTCCCAAAGAGAGGCCCTTTTCAGTTGAG
ACTCTGCTTAAGAGAAGATCAAAGTTAAAGCTCTGGGGTCAGGGGAGGGGCCGGGGCAGG
AAACTACCTCTGGCTTAATCTTTTAAAGCCAGTAGGAACCTTCTTGAGGAGATAGGTGAGC
CTGACATCCCTGTGGCCTTGCCCAAGGGCTCTGCTGCTTCTTGAGTCAAGTCTGCGAGCT
GATGGGGGCTGGGGCCCCAGGCGTCAGCCTCCAGAGGGACAGCTGAGCCCCCTGCCTTGGC
TCCAGGTTGGTAGAAGCAGCCGAAGGGCTCTGACAGTGGCCAGGGACCCCTGGGTCCCCCA
GGCCTGCAGATGTTTCTATGAGGGGCGAGAGCTCCTTGGTACATCCATGTGTGGCTCTGCTCC
ACCCCTGCGCACCCAGAGCCCTGGGGGGTGGTCTCCATGCTGCCACCTGCGACCTCGGCT
TTCTGTGCGGCTCCACACAAATCAGCCCCAGAAGGCCCGGGGCCCTTGGCTCTGTTT
TATAAAACACCTCAAGCAGCACTGCAGTCTCCCATCTCTCTGTTGGGCTAAGCATCACGCCT
CCACGTGTGTGTGTTGGTTGGCAGCAAGGTGATCCAGACCCCTCTGCCCCCAGTGCCCT
CATCCAGGCCCTTGACCACTAGCCTGAGAGGGGCTTTTTCTAGGCTTTCAGAGCAGGGGAGAG
CTGGAAGGGGCTAGAAAGCTCCGCTGTGTCTTCTCAGGCTCTGTGAGCTCTCAGTCTGCTG
AGACCAGAGTCAAGAGGAAGTACACGTCCCAATCACCCGTGTAGGATTCACTCTCAGGAGC
TGGGTGGCAGGAGAGGCAATAGCCCCGTGTGGCAATTGCAGGACCAGCTGGAGCAGGGTTGGC
GTGTCTCCACGGTGTCTCGCCCTGCCCATGGCCACCCAGACTCTGATCTCCAGGAACCCC
ATAGCCCTCTCCACCTCACCCTATGTTGATGCCAGGGTCACTTGTCTACCCGCTGGGCC
CCAAACCCCGCTGCTCTCTTCTTCCCCCATCCCCACCTGGTTTGACTAATCTCTGC
TTCCCTCTCTGGGCTTGGCTGCCGGGATCTGGGGTCCCTAAGTCCCTCTCTTAAAGAACCT
CTGCGGGTCACTGCTGAAGCCGAGTTGCTGTGGGCGTGCCCGAAGCAGAGCGCCACACTC
GCTGCTTAAGTCCCCAGCTCTTCCAGAAACATAAAGTCAAGATTGTGTTTCAA

FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234
><subunit 1 of 1, 281 aa, 1 stop
><MW: 31743, pI: 6.83, NX(S/T): 1
MSSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELFSPPDHAERAEQHEKYRP
SQDQGLPASRCLCCDPGTSMPATAVPQINITILKGEKGDRGDRGLQGYKGTGSAGARGH
TGPKGQKGSMSGAPGERCKSHYAASFVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMTGKFY
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDRSIMQSSQLMLELREQDQVWV
RLYKGERENAIFSEELDTYITFSGYLVKHATEP

Signal sequence.

amino acids 1-25

N-glycosylation site.

amino acids 93-97

N-myristoylation sites.

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

Amidation site.

amino acids 150-154

Cell attachment sequence.

amino acids 104-107

FIGURE 31

GCGGAGCATCCGCTGCGGTCTCTGCGGAGACCCCGCGCGGATTGCGCGGTCTCTCCCGCGG
 GCGGACAGAGCTGTCTCTGCGACCTGGATTGGCAGCAGGGGCGCCGGGGTCTCTCTGACGCCA
 GAGAGAAATCTCATCATCTGTGCAGCCTTCTTAAAGCAAACCTAAGACCAAGAGGGAGGATTAT
 CCTTGACCTTTGAAGACCAAACTAACTGAAATTTAAATATGTCTCTCGGGGAGAAAGGGAG
 CTTGACTTACACTTTGGTAATAATTTGCTTCTGACACTAAGGCTGTCTGTAGTCAGAATT
 GCCTCAAAAAGAGTCTAGAAGATGTTGTCTTGACATCCAGTCATCTCTTTCTAAGGGAATC
 AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAAATCTTGCTGTTCAAC
 AAAAAACATATCAGGGGACAAAGCATGTAACTTGATGATCTTCGACACTCGAAAAACAGCTA
 GACAACCAACTGCTACCTATTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACAGCA
 AAAGGACTTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
 CCAAGAGTTACCCAGGAAGATTCTCTCTTACATGGCCAATTTTCAAGCAGTCACTCCCC
 TAGCCCATCATCACAGATTATTCAAGGCCACCGATATCTCATGGAGAGACACTTTCT
 CAGAAGTTTGGATCCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAATTTTCTCTGATCAAGAAA
 TAGCTCATCTGCTGCTGAAATGTGAGTGCGCTCCAGCTACGGTGGCAGTTGCTTCTCCA
 CATACCACCTCGGCTACTCCAAAGCCCGCCACCCTTCTACCCCAATGCTTCAGTGACACC
 TTCTGGGACTTCCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC
 AGCCTCCACAGCCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG
 GCTAACACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA
 AACCATACCGTTTACAGAAATCTCCAACCTTAACTTTGAACACAGGGAATGTGTATAACCCCTA
 CTGCACCTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTCTGGGAAGGT
 AGGGAGGCCAGTCCAGGCAGTTCTCTCCAGGGCAGTGTTCAGAAAAATCAGTACGGCCTTCC
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGCTCCTGTTCTGGTGATAGGCC
 TCGTCTCTCTGGGTAGAATCCTTTCCGAATCACTCCGCAGGAAACGTTACTCAAGACTGGAT
 TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTCGGTGTCTCTTAATTCATT
 TAGTAACCAAGAACCCCAATGCAATGAGTTTCTGCTGACTTGCTAGCTTTAGCAGGAGGTTG
 TATTTTGAAGACAGGAAATGCCCCCTTCTGCTTTCCTTTTTTTTTTTTGGAGACAGAGTCTT
 GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGCAACCTCCGCTCTC
 CTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA
 CCACACTGGGTGATTTTGTATTTTGTATTTTGTAGTAGAGACGGGGTTTCCACATGTTGGTCAGGCTG
 GTCTCAAACCTCTGACCTAGTGATCCACCTCCTCGGCCTCCCAAAGTGCTGGGATTACAGG
 CATGAGCCACCACAGCTGGCCCCCTTCTGTTTTATGTTTGGTTTTTGAAGGAATGAAGTG
 GGAACCAAATTAGGTAATTTTGGGTAATCTGTCTTAAATATTAGCTAAAAACAAAGCTCT
 ATGTAAGTAATAAAGTATAATTGCCATATAAATTTCAAATTCACATGCTTTTATGCAAAA
 GAAACAGGTTAGGACATCTAGGTTCCAATTCATTACATTTCTGGTTCCAGATAAAATCAAC
 TGTTTATATCAATTTCTAATGGATTGCTTTTCTTTTATATGAGATTCCTTTAAACCTTATT
 CCAGATGTAGTTCCTTCCAATTAATATTTGAATAAATCTTTTGTACTCAA

FIGURE 32

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MPFGGEGSLTYTLVIIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEI AHLLPENVSALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSV
PENQYGLPFEKWLIGSLLFGVLFVLVIGLVLLGRILSESLRRKRYSRLDYLINGIYVDI

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 33

GCGGCACCTGGAAGATGCGCCCATTTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTC
GCCTCCTTGTGTGCCTGGTATTTCGGGGTACCTGCTCGCAGAGCTCATTCAGATGCACCCCT
GTCCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCTC~~CAA~~AGCTCCAGTCC
CCAAAAGGCCAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTA
CTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGG
AGAACAGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAAC~~TGG~~GA
ATGTGACAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAG
TTTATTCAGAGTGCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCAC
AAGACTGAATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACA
TGAAATTCAGGTCTAGCTGGGTATTTATTGCGAGCAAAAGGCTTGGAAC~~TCC~~CTTCGAAATT
CAGAGAGAAAAGATCAACCACTCTGATGCTAAGAACAACAGATATTCTGGCTGGCCTGCAGA
GATCCAGATAGAAGGCTGCATACCCAAAGAACGAAGCTGA~~CA~~CTGCAGGGTCTGAGTAAAT
GTGTTCTGTATAAACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTCTAAATCCAACA
GCCCATATTTGATGAGTATTTTGGGTTTGTGTAAACCAATGAACATTGCTAGTTGTATCA
AATCTTGGTACGCAGTATTTTTATACCAGTATTTTATGTAGTGAAGATGTCAATTAGCAGGA
AACTAAAATGAATGGAATTCCTTAAAAAAAAA

FIGURE 34

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46777
><subunit 1 of 1, 235 aa, 1 stop
><MW: 25982, pI: 9.09, NX(S/T): 2
MRPLAGGLLKVVFFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVVKRQK
CDHWTPCPSDITYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT
RCFDMEYEGDNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDAKNAIEALGSKEIRNMKFRS
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCIPKERS

Signal sequence.

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125